Rec'd PCT/PTO 04 OCT 2005



Sequence Listing

```
<110> Sode,
<120> Glucose Dehydrogenase
<130> 3691-0114PUS1
<140> US 10/520,126
<141> 2005-01-03
<150> PCT/JP03/08418
<151> 2002-07-02
<150> JP 2003-71760
<151> 2003-03-17
<150> JP 2002-196177
<151> 2002-07-04
<160> 19
<170> PatentIn version 3.3
<210> 1
<211> 454
<212> PRT
<213> Acinetobacter calcoaceticus
<400> 1
Asp Val Pro Leu Thr Pro Ser Gln Phe Ala Lys Ala Lys Ser Glu Asn
Phe Asp Lys Val Ile Leu Ser Asn Leu Asn Lys Pro His Ala Leu
                                 25
Leu Trp Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly
Lys Ile Leu Arg Val Asn Pro Glu Ser Gly Ser Val Lys Thr Val Phe
Gln Val Pro Glu Ile Val Asn Asp Ala Asp Gly Gln Asn Gly Leu Leu
                     70
                                         75
                                                              80
Gly Phe Ala Phe His Pro Asp Phe Lys Asn Asn Pro Tyr Ile Tyr Ile
                                     90
Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn
            100
                                105
                                                     110
Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Ser Thr Asp Thr Leu
                            120
                                                 125
Glu Lys Pro Val Asp Leu Leu Ala Gly Leu Pro Ser Ser Lys Asp His
                        135
Gin Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
                    150
Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
Gln Ala Gln His Thr Pro Thr Gln Gln Glu Leu Asn Gly Lys Asp Tyr
            180
                                185
His Thr Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Ile
                            200
Pro Lys Asp Asn Pro Ser Phe Asn Gly Val Val Ser His Ile Tyr Thr
```

```
215
                                              220
 Leu Gly His Arg Asn Pro Gln Gly Leu Ala Phe Thr Pro Asn Gly Lys
                     230
                                          235
 Leu Leu Gln Ser Glu Gln Gly Pro Asn Ser Asp Asp Glu Ile Asn Leu
                                      250
· Ile Val Lys Gly Gly Asn Tyr Gly Trp Pro Asn Val Ala Gly Tyr Lys
                                 265
             260
                                                      270
 Asp Asp Ser Gly Tyr Ala Tyr Ala Asn Tyr Ser Ala Ala Ala Asn Lys
                             280
 Ser Ile Lys Asp Leu Ala Gln Asn Gly Val Lys Val Ala Ala Gly Val
                         295
 Pro Val Thr Lys Glu Ser Glu Trp Thr Gly Lys Asn Phe Val Pro Pro
                     310
                                          315
 Leu Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp Pro
                 325
                                      330
 Thr Cys Gly Glu Met Thr Tyr Ile Cys Trp Pro Thr Val Ala Pro Ser
                                 345
 Ser Ala Tyr Val Tyr Lys Gly Gly Lys Lys Ala Ile Thr Gly Trp Glu
                             360
                                                  365
 Asn Thr Leu Leu Val Pro Ser Leu Lys Arg Gly Val Ile Phe Arg Ile
                         375
                                              380
 Lys Leu Asp Pro Thr Tyr Ser Thr Thr Tyr Asp Asp Ala Val Pro Met
                     390
                                          395
 Phe Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Asp Gly
                                      410
 Asn Val Leu Tyr Val Leu Thr Asp Thr Ala Gly Asn Val Gln Lys Asp
                                 425
 Asp Gly Ser Val Thr Asn Thr Leu Glu Asn Pro Gly Ser Leu Ile Lys
         435
                             440
 Phe Thr Tyr Lys Ala Lys
     450
 <210> 2
 <211> 1612
 <212> DNA
 <213> Acinetobacter calcoaceticus
 <400> 2
 agctactttt atgcaacaga gcctttcaga aatttagatt ttaatagatt cgttattcat 60
 cataatacaa atcatataga gaactcgtac aaacccttta ttagaggttt aaaaattctc 120
 ggaaaatttt gacaatttat aaggtggaca catgaataaa catttattgg ctaaaattgc 180
 tttattaage getgtteage tagttacaet eteageattt getgatgtte etetaaetee 240
 atctcaattt gctaaagcga aatcagagaa ctttgacaag aaagttattc tatctaatct 300
 aaataagccg catgctttgt tatggggacc agataatcaa atttggttaa ctgagcgagc 360
 aacaggtaag attotaagag ttaatocaga gtogggtagt gtaaaaacag tttttcaggt 420
 accagagatt gtcaatgatg ctgatgggca gaatggttta ttaggttttg ccttccatcc 480
 tgattttaaa aataatcctt atatctatat ttcaggtaca tttaaaaaatc cgaaatctac 540
 agataaagaa ttaccgaacc aaacgattat tcgtcgttat acctataata aatcaacaga 600
 tacgctcgag aagccagtcg atttattagc aggattacct tcatcaaaag accatcagtc 660
 aggtcgtctt gtcattgggc cagatcaaaa gatttattat acgattggtg accaagggcg 720
 taaccagctt gcttatttgt tcttgccaaa tcaagcacaa catacgccaa ctcaacaaga 780
 actgaatggt aaagactatc acacctatat gggtaaagta ctacgcttaa atcttgatgg 840
 aagtattcca aaggataatc caagttttaa cggggtggtt agccatattt atacacttgg 900
 acatogtaat cogcagggot tagoattoac tocaaatggt aaattattgc agtotgaaca 960
 aggeceaaae tetgaegatg aaattaaeet eattgteaaa ggtggeaatt atggttggee 1020
 gaatgtagca ggttataaag atgatagtgg ctatgcttat gcaaattatt cagcagcagc 1080
```

```
caataagtca attaaggatt tagctcaaaa tggagtaaaa gtagccgcag gggtccctgt 1140
 gacgaaagaa totgaatgga otggtaaaaa otttgtooca ocattaaaaa otttatata 1200
 cgttcaagat acctacaact ataacgatcc aacttgtgga gagatgacct acatttgctg 1260
 gccaacagtt gcaccgtcat ctgcctatgt ctataagggc ggtaaaaaag caattactgg 1320
 ttgggaaaat acattattgg ttccatcttt aaaacgtggt gtcattttcc gtattaagtt 1380
- agatccaact tatagcacta cttatgatga cgctgtaccg atgtttaaga gcaacaaccg 1440
 ttatcgtgat gtgattgcaa gtccagatgg gaatgtctta tatgtattaa ctgatactgc 1500
 cggaaatgtc caaaaagatg atggctcagt aacaaataca ttagaaaacc caggatctct 1560
 cattaagttc acctataagg ctaagtaata cagtcgcatt aaaaaaccga tc
 <210> 3
 <211> 8
 <212> PRT
 <213> Acinetobacter calcoaceticus
 <220>
 <221> misc feature
 <222>
        (4)..(5)
 <223> Xaa can be any amino acid provided that when Xaa at pos. 4 is Gln, then
        Xaa at pos. 5 is not Leu
 <400> 3
 Gly Arg Asn Xaa Xaa Ala Tyr Leu
 <210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <223> synthetic primer for point mutation
 <400> 4
 ataagcaagc gggttacgcc c 21
 <210> 5
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic primer for point mutation
 <400> 5
 caaataagca agcccgttac gcccttg 27
 <210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
```

```
<223> synthetic primer for point mutation
<400> 6
caaataagca gcctggttac g 21
<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 7
gaacaaataa gcaccctggt tacgccc 27
<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 8
cctgactgat gttcttttga tgaagg 26
<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 9
catctttttg gacagttccg gcagtat 27
<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 10
caaataagca agcaggttac gcccttg 27
<210> 11
<211> 27
<212> DNA
```

```
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 11
caaataagca agaaagttac gcccttg 27
<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 12
caaataagca aggctgttac gcccttg 27
<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 13
caaataagca aggttgttac gcccttg 27
<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 14
caaataagca agatcgttac gcccttg 27
<210> 15
<211> 27
<212> DŃA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 15
caaataagca agttcgttac gcccttg 27
```

```
<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 16
caaataagca agtttgttac gcccttg 27
<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence
<223> synthetic primer for point mutation
<400> 17
gaacaaataa gccatctggt tacgccc 27
<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic primer for point mutation
<400> 18
gaacaaataa gctttctggt tacgccc 27
<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence
<223> synthetic primer for point mutation
<400> 19
gaacaaataa gcccactggt tacgccc 27
```